

20070821_seq.txt
SEQUENCE LISTING

<110> Wei, Xin
Gariepy , Jean

<120> LIBRARY OF HETEROMERIC TOXIN MUTANTS, AND METHODS OF USING SAME

<130> 34104-0082

<160> 7

<170> PatentIn version 3.2

<210> 1
<211> 299
<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<223> Wild type SLT-1 A chain

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Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr
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Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp
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Ser	Gly	Ser	Gly	Asp	Asn	Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp
	50					55					60				

Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn
65					70					75					80

Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr
				85					90					95	

Arg	Phe	Ala	Asp	Phe	Ser	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val
			100					105					110		

Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly
		115					120					125			

Ile	Ser	Arg	Thr	Gly	Met	Gln	Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser
	130					135					140				

Tyr	Leu	Asp	Leu	Met	Ser	His	Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val
145					150					155					160

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Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg
165 170 175

Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser
180 185 190

Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn
195 200 205

Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser
210 215 220

Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly
225 230 235 240

Ser Val Ala Leu Ile Leu Asn Cys His His His Ala Ser Arg Val Ala
245 250 255

Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro Ala Asp Gly Arg
260 265 270

Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu
275 280 285

Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser
290 295

<210> 2
<211> 32
<212> DNA
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<220>
<223> Primer

<400> 2
gttactgtga cagctgaagc ttacgtttt cg

32

<210> 3
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<213> Artificial

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<210> 4

<211> 302
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<223> SLT-1 A Chain lib#3 protein sequence (SAM3)

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Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr
 20 25 30

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln
 35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser
 50 55 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu
 65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr
 85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala
 100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser
 115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg
 130 135 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp
 145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala
 165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln
 180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser
 195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg
 210 215 220

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Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val
225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala
245 250 255

Leu Ile Leu Asn Cys His His His Ile Tyr Ser Asn Lys Leu Met Ala
260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro
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Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu
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<212> PRT
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<223> SLT-1 A Chain lib#5 protein sequence (SAM5)

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Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr
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Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln
35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser
50 55 60

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu
65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr
85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala
100 105 110

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser
115 120 125

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Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg
130 135 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp
145 150 155 160

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala
165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln
180 185 190

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser
195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg
210 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val
225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala
245 250 255

Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Leu Ile Ala
260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro
275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp
290 295 300

Ser Ser Thr Leu Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser
305 310 315

<210> 6

<211> 7

<212> PRT

<213> Artificial

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<223> First melanoma active insert

<400> 6

Ile Tyr Ser Asn Lys Leu Met
1 5

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<210> 7
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Second melanoma active insert

<400> 7

Ala Ala Phe Ala Asp Leu Ile
1 5